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SEQUENCE LISTING

<110> INSERM

<120> Infectious pestivirus pseudo-particles containing functional E1 and E2 glycoproteins

<130> BET 03/P0182 PCT

<160> 26

<170> PatentIn version 3.2

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11

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12573

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 <212> PRT
 <213> Bovine viral diarrhea virus

<400> 2

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Asp Arg Leu Glu Arg Gly Lys Met Lys Ile Val Pro Lys Glu Ser Glu
 20 25 30

Lys Asp Ser Lys Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly
 35 40 45

Val Lys Tyr Gln Val Arg Lys Lys Gly Lys Thr Lys Ser Lys Asn Thr
 50 55 60

Gln Asp Gly Leu Tyr His Asn Lys Asn Lys Pro Gln Glu Ser Arg Lys
 65 70 75 80

Lys Leu Glu Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu
 85 90 95

Phe Gln Val Thr Met Gly
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<210> 3
 <211> 227
 <212> PRT
 <213> Bovine viral diarrhea virus

<400> 3

Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu Gly Ile
 1 5 10 15

Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile
 20 25 30

Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala Thr Asp
 35 40 45

Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu Lys Thr
 50 55 60

... 12

Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys His Gly
65 70 75 80

Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met Asn Arg
85 90 95

Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys Ala Val
100 105 110

Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr Gln Ala
115 120 125

Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe
130 135 140

Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu Ile Ala
145 150 155 160

Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met Phe Gln
165 170 175

Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu Glu Gly
180 185 190

Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys Gln Leu
195 200 205

Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp Phe Gly
210 215 220

Ala Tyr Ala
225

<210> 4
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<212> PRT
<213> Bovine viral diarrhea virus

<400> 4

Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr
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Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val
20 25 30

Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His

13

35

40

45

Glu Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val
50 55 60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu
65 70 75 80

His Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys
85 90 95

Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro
100 105 110

Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp
115 120 125

Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln
130 135 140

Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp
145 150 155 160

Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val
165 170 175

Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly
180 185 190

Val Gln Gly
195

<210> 5

<211> 374

<212> FRT

<213> Bovine viral diarrhea virus

<400> 5

His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys Asp Glu
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20 25 30

Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala Trp Cys
35 40 45

14

Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu Thr Arg
50 55 60

Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val Val Phe
65 70 75 80

Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu Met Asn
85 90 95

Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro Ile Val
100 105 110

Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe Gln Met
115 120 125

Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser Phe Asn
130 135 140

Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg Ser Lys
145 150 155 160

Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu Gly Glu
165 170 175

Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val Pro Gly
180 185 190

Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys Trp Cys
195 200 205

Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro Ile Gly
210 215 220

Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp Ser Thr
225 230 235 240

Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr Leu Lys
245 250 255

Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp Thr Lys
260 265 270

Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser Glu Gly
275 280 285

15

Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr Leu Lys
 290 295 300

Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu
 305 310 315 320

Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp His His
 325 330 335

Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala Leu Leu
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Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val Leu Ser
 355 360 365

Glu Gln Lys Ala Leu Gly
 370

<210> 6
 <211> 70
 <212> PRT
 <213> Bovine viral diarrhea virus

<400> 6

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His Asn Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu
 20 25 30

Leu Arg Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile
 35 40 45

Leu Val Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile
 50 55 60

Gly Asp Val Val Lys Ala
 65 70

<210> 7
 <211> 12301
 <212> LNA
 <213> Swine fever virus

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 Ser Asp Asp Gly Ala Ser
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 gga agt aaa gag aag aag cca gat agg atc aac aaa ggc aaa tta aza 913
 Gly Ser Lys Glu Lys Lys Pro Asp Arg Ile Asn Lys Gly Lys Leu Lys
 10 15 20
 ata gcc cca aaa gag cat gag aag gac agc aga act aag cca cct gag 991
 Ile Ala Pro Lys Glu His Glu Lys Asp Ser Arg Thr Lys Pro Pro Asp
 25 30 35

17

gct acg att gta gtg gaa gga gta aaa tac cag gtt aaa aag aag ggt Ala Thr Ile Val Val Glu Gly Val Lys Tyr Gln Val Lys Lys Lys Gly 40 45 50	1039
aaa gtt aaa gga aag agt acc caa gac ggc ctg tac cac aac aag aat Lys Val Lys Gly Lys Ser Thr Gln Asp Gly Leu Tyr His Asn Lys Asn 55 60 65 70	1087
aaa cca cca gaa tct agg aag aaa tta gaa aaa gcc cta ttg gca tgg Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala Trp 75 80 85	1135
ggg gta ata gca att atg ttg tac caa cca gtt gaa gcc gaa aat ata Ala Val Ile Ala Ile Met Leu Tyr Gln Pro Val Glu Ala Glu Asn Ile 90 95 100	1183
act caa tgg aac ctg agt gac aac ggc act aat ggt atc cag cat gct Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile Gln His Ala 105 110 115	1231
atg tac ctt aga ggg gtt agc agg agc ttg cat ggg atc tgg ccg gaa Met Tyr Leu Arg Gly Val Ser Arg Ser Leu His Gly Ile Trp Pro Glu 120 125 130	1279
aaa ata tgc aaa gga gtc ccc acc tac ctg gcc aca gac acg gaa ctg Lys Ile Cys Lys Gly Val Pro Thr Tyr Leu Ala Thr Asp Thr Glu Leu 135 140 145 150	1327
aaa gaa ata cag gga atg atg gat gcc agc gag ggg aca aac tat acg Lys Glu Ile Gln Gly Met Met Asp Ala Ser Glu Gly Thr Asn Tyr Thr 155 160 165	1375
tgc tgt aag tta cag aga cat gaa tgg aac aaa cat gga tgg tgt aac Cys Cys Lys Leu Gln Arg His Glu Trp Asn Lys His Gly Trp Cys Asn 170 175 180	1423
ggg tac aat ata gac ccc tgg ata cag ttg atg aat aga acc caa gca Trp Tyr Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg Thr Gln Ala 185 190 195	1471
aac ttg gca gaa ggc cct ccg gcc aag gag tgc gct gtg act tgc agg Asn Leu Ala Glu Gly Pro Pro Ala Lys Glu Cys Ala Val Thr Cys Arg 200 205 210	1519
tac gat aaa gat gct gac atc aac gtg gtc acc cag gcc aga aac agg Tyr Asp Lys Asp Ala Asp Ile Asn Val Val Thr Gln Ala Arg Asn Arg 215 220 225 230	1567
cca aca acc ctg acc ggt tgc aag aaa gga aaa aat ttt tct ttt gcg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser Phe Ala 235 240 245	1615
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atc ttg tat ggg gat cat gag tgc ggc agt ttg ctt cag gac acg gct Ile Leu Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln Asp Thr Ala 265 270 275	1711

18

ctg tac cta gtg gat gga atg acc aac act ata gag aat gcc aga cag Leu Tyr Leu Val Asp Gly Met Thr Asn Thr Ile Glu Asn Ala Arg Gln 280 285 290	1759
gga gca gcg agg gta aca tct tgg ctc ggg agg caa ctc agc act gcc Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu Ser Thr Ala 295 300 305 310	1807
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cta tgg cct tac tgt aat gta aca agc aaa ata ggg tac ata tgg tac Leu Ser Pro Tyr Cys Asn Val Thr Ser Lys Ile Gly Tyr Ile Trp Tyr 330 335 340	1903
act aac aac tgc acc ccg gct tgc ctc ccc aaa aat aca aag ata ata Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile 345 350 355	1951
ggc ccc gga aaa ttt gac act aac gcg gaa gac gga aag att ctc cat Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His 360 365 370	1999
gag atg ggg ggt cac cta tca gaa ttt ctg ctg ctc tcl ctg gtt gtt Glu Met Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Val 375 380 385 390	2047
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cac tac atg att cct caa tcc cat gaa gaa cct gaa ggc tgc gac aca His Tyr Met Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr 410 415 420	2143
aac cag ctg aat cta aca gtc gaa ctc agg act gaa gac gta ata ccg Asn Gln Leu Asn Leu Thr Val Glu Leu Arg Thr Glu Asp Val Ile Pro 425 430 435	2191
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Ala Gln Gly Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser 520 525 530	
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aaa ggt gaa cca gtg gtc tac acg ggg ggg cta gta aza caa tgc aga Lys Gly Glu Pro Val Val Tyr Thr Gly Gly Leu Val Lys Gln Cys Arg 715 720 725	3055
tgg tgt ggc ttc gac ttc aat gag ccc gac gga ctc ccg cac tac ccc Trp Cys Gly Phe Asp Phe Asn Glu Pro Asp Gly Leu Pro His Tyr Pro 730 735 740	3103
ata ggt aag tgc atc ttg gta aat gag aca ggt tac aga ata gta gat Ile Gly Lys Cys Ile Leu Val Asn Glu Thr Gly Tyr Arg Ile Val Asp 745 750 755	3151
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775	780	785	790
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Glu Arg Leu Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser			
	795	800	805
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Ala Gly Pro Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Ala Lys Thr			
	810	815	820
ttg aag aac aag tac tat gag ccc agg gac agc tac ttc cag caa tat			3391
Leu Lys Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr			
	825	830	835
atg ctt aag ggc gag tat cag tac tgg ttt gac ctg gac gtg act gac			3439
Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Asp Val Thr Asp			
	840	845	850
cgc cac tca gat tac ttc gca gaa ttt gtc gtc ttg gta gtg gta gca			3487
Arg His Ser Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala			
	855	860	865
ctg tta gga gga aga tat gtc ctg tgg cta ata gtg acc tac ata gtt			3535
Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Val			
	875	880	885
cta aca gaa caa ctc gcc gct ggt tta cca ttg ggc cag ggt gag gta			3583
Leu Thr Glu Gln Leu Ala Ala Gly Leu Pro Leu Gly Gln Gly Glu Val			
	890	895	900
gtg ttg ata ggg aac tta att acc cac aca gac att gag gtc gta gta			3631
Val Leu Ile Gly Asn Leu Ile Thr His Thr Asp Ile Glu Val Val Val			
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tat ttc tta cta ctc tat ttg gtc atg agg gat gag cct ata aag aaa			3679
Tyr Phe Leu Leu Leu Tyr Leu Val Met Arg Asp Glu Pro Ile Lys Lys			
	920	925	930
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Trp Ile Leu Leu Leu Phe His Ala Met Thr Asn Asn Pro Val Lys Thr			
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Ile Thr Val Ala Leu Leu Met Val Ser Gly Val Ala Lys Gly			
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<210> 8
 <211> 99
 <212> FRT
 <213> Swine fever virus

<400> 8

Ser Asp Asp Gly Ala Ser Gly Ser Lys Glu Lys Lys Pro Asp Arg Ile
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Asn Lys Gly Lys Leu Lys Ile Ala Pro Lys Glu His Glu Lys Asp Ser
 20 25 30

Arg Thr Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Val Lys Tyr
 35 40 45

Gln Val Lys Lys Lys Gly Lys Val Lys Gly Lys Ser Thr Gln Asp Gly
 50 55 60

Leu Tyr His Asn Lys Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu
 65 70 75 80

Lys Ala Leu Leu Ala Trp Ala Val Ile Ala Ile Met Leu Tyr Gln Pro
 85 90 95

Val Glu Ala

<210> 9
 <211> 227
 <212> PRT
 <213> Swine fever virus
 <400> 9

Glu Asn Ile Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Asn Gly Ile
 5 10 15

Gln His Ala Met Tyr Leu Arg Gly Val Ser Arg Ser Leu His Gly Ile
 20 25 30

Trp Pro Glu Lys Ile Cys Lys Gly Val Pro Thr Tyr Leu Ala Thr Asp
 35 40 45

Thr Glu Leu Lys Glu Ile Gln Gly Met Met Asp Ala Ser Glu Gly Thr
 50 55 60

Asn Tyr Thr Cys Cys Lys Leu Gln Arg His Glu Trp Asn Lys His Gly
 65 70 75 80

Trp Cys Asn Trp Tyr Asn Ile Asp Pro Trp Ile Gln Leu Met Asn Arg
 85 90 95

Thr Gln Ala Asn Leu Ala Glu Gly Pro Pro Ala Lys Glu Cys Ala Val
 100 105 110

Thr Cys Arg Tyr Asp Lys Asp Ala Asp Ile Asn Val Val Thr Gln Ala
 115 120 125

Arg Asn Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe
 130 135 140

Ser Phe Ala Gly Thr Val Ile Glu Gly Pro Cys Asn Phe Asn Val Ser
 145 150 155 160

Val Glu Asp Ile Leu Tyr Gly Asp His Glu Cys Gly Ser Leu Leu Gln
 165 170 175

Asp Thr Ala Leu Tyr Leu Val Asp Gly Met Thr Asn Thr Ile Glu Asn
 180 185 190

Ala Arg Gln Gly Ala Ala Arg Val Thr Ser Trp Leu Gly Arg Gln Leu
195 200 205

Ser Thr Ala Gly Lys Arg Leu Glu Gly Arg Ser Lys Thr Trp Phe Gly
210 215 220

Ala Tyr Ala
225

<210> 10
<211> 195
<212> PRT
<213> Swine fever virus

<400> 10

Leu Ser Pro Tyr Cys Asn Val Thr Ser Lys Ile Gly Tyr Ile Trp Tyr
1 5 10 15

Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
20 25 30

Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
35 40 45

Glu Met Gly Gly His Leu Ser Glu Phe Leu Leu Leu Ser Leu Val Val
50 55 60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Ala Leu Tyr Leu Ile Leu
65 70 75 80

His Tyr Met Ile Pro Gln Ser His Glu Glu Pro Glu Gly Cys Asp Thr
85 90 95

Asn Gln Leu Asn Leu Thr Val Glu Leu Arg Thr Glu Asp Val Ile Pro
100 105 110

Ser Ser Val Trp Asn Val Gly Lys Tyr Val Cys Val Arg Pro Asp Trp
115 120 125

Trp Pro Tyr Glu Thr Lys Val Ala Leu Leu Phe Glu Glu Ala Gly Gln
130 135 140

Val Val Lys Leu Ala Leu Arg Ala Leu Arg Asp Leu Thr Arg Val Trp
145 150 155 160

Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Ile Lys Val Leu
165 170 175

Arg Gly Gln Ile Val Gln Gly Val Ile Trp Leu Leu Leu Val Thr Gly
180 185 190

Ala Gln Gly
195

<210> 11
<211> 373
<212> PRT
<213> Swine fever virus
<400> 11

Arg Leu Ala Cys Lys Glu Asp Tyr Arg Tyr Ala Ile Ser Ser Thr Asn
1 5 10 15

Glu Ile Gly Leu Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp Lys Glu
20 25 30

Tyr Asn His Asp Leu Gln Leu Asn Asp Gly Thr Val Lys Ala Ile Cys
35 40 45

Val Ala Gly Ser Phe Lys Val Ile Ala Leu Asn Val Val Ser Arg Arg
50 55 60

Tyr Leu Ala Ser Leu His Lys Glu Ala Ser Leu Thr Ser Val Thr Phe
65 70 75 80

Glu Leu Leu Phe Asp Gly Thr Asn Pro Ser Thr Glu Glu Met Gly Asp
85 90 95

Asp Phe Gly Phe Gly Leu Cys Pro Phe Asp Thr Ser Pro Val Val Lys
100 105 110

Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Tyr Leu Val
115 120 125

Cys Pro Ile Gly Trp Thr Gly Val Ile Glu Cys Thr Ala Val Ser Pro
130 135 140

Thr Thr Leu Arg Thr Glu Val Val Lys Thr Phe Arg Arg Asp Lys Pro
145 150 155 160

Phe Pro His Arg Met Asp Cys Ala Thr Thr Thr Val Glu Asn Gly Asp
165 170 175

29

Leu Phe Tyr Cys Lys Leu Gly Gly Asn Trp Thr Cys Val Lys Gly Glu
 180 185 190

Pro Val Val Tyr Thr Gly Gly Leu Val Lys Gln Cys Arg Trp Cys Gly
 195 200 205

Phe Asp Phe Asn Glu Pro Asp Gly Leu Pro His Tyr Pro Ile Gly Lys
 210 215 220

Cys Ile Leu Val Asn Glu Thr Gly Tyr Arg Ile Val Asp Ser Thr Asp
 225 230 235 240

Cys Asn Arg Asp Gly Val Val Ile Ser Thr Asp Gly Ser His Glu Cys
 245 250 255

Leu Ile Gly Asn Thr Thr Val Lys Val His Ala Ser Asp Glu Arg Leu
 260 265 270

Gly Pro Met Pro Cys Arg Pro Lys Glu Ile Val Ser Ser Ala Gly Pro
 275 280 285

Val Arg Lys Thr Ser Cys Thr Phe Asn Tyr Ala Lys Thr Leu Lys Asn
 290 295 300

Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys
 305 310 315 320

Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Asp Val Thr Asp Arg His Ser
 325 330 335

Asp Tyr Phe Ala Glu Phe Val Val Leu Val Val Val Ala Leu Leu Gly
 340 345 350

Gly Arg Tyr Val Leu Trp Leu Ile Val Thr Tyr Ile Val Leu Thr Glu
 355 360 365

Gln Ile Ala Ala Gly
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<210> 12
 <211> 70
 <212> PRT
 <213> Swine fever virus

<400> 12

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His Thr Asp Ile Glu Val Val Val Tyr Phe Leu Leu Leu Tyr Leu Val
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Met Arg Asp Glu Pro Ile Lys Lys Trp Ile Leu Leu Leu Phe His Ala
 35 40 45

Met Thr Asn Asn Pro Val Lys Thr Ile Thr Val Ala Leu Leu Met Val
 50 55 60

Ser Gly Val Ala Lys Gly
 65 70

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 <212> DNA
 <213> Border disease virus

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 Ser Asp Asp Asn Lys Ser
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 Glu Lys Thr Asn Glu Lys Lys Pro Asp Arg Val Arg Arg Gly Ala Met
 10 15 20
 aag atc aca ccc aaa gag agt gag aag gat agt aga tct aag cca cct 990
 Lys Ile Thr Pro Lys Glu Ser Glu Lys Asp Ser Arg Ser Lys Pro Pro
 25 30 35
 gac gca act ata gta gta gaa ggc ata aaa tac cag gta aag aag aaa 1038
 Asp Ala Thr Ile Val Val Glu Gly Ile Lys Tyr Gln Val Lys Lys Lys
 40 45 50
 gga aag gtg aag ggc aag aac aca caa gat ggc tta tac cac aac aag 1086
 Gly Lys Val Lys Gly Lys Asn Thr Gln Asp Gly Leu Tyr His Asn Lys
 55 60 65 70
 aac aag cca cct gag tct aga aag aan ttg gag aaa ccc cta ctg gct 1134
 Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu Ala
 75 80 85
 tgg gct ata ata gca atc ttc atg tgg gaa ccc gta gca cca gag aat 1192
 Trp Ala Ile Ile Ala Ile Phe Met Trp Glu Pro Val Ala Pro Glu Asn
 90 95 100
 gtg aca caa tgg aac cta agt gac aac ggg act acc ggc atc caa ctc 1230
 Val Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Thr Gly Ile Gln Leu
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 cta atg ttc caa aga ggt gtt aac aga agc ctg cac ggt att tgg cct 1278
 Leu Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp Pro
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 gaa aag ata tgt aca gga glg ccc acg cac tng gca aca gat gca gag 1326
 Glu Lys Ile Cys Thr Gly Val Pro Thr His Leu Ala Thr Asp Ala Glu
 135 140 145 150
 ttg aaa gga att caa ggg atg atg gat gct agt gaa aag act aat tac 1374
 Leu Lys Gly Ile Gln Gly Met Met Asp Ala Ser Glu Lys Thr Asn Tyr
 155 160 165

32

aca tgc tgc aga ctt cag aga cac gaa tgg aac aag tac ggg tgg tgc 1422
 Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys Tyr Gly Trp Cys
 170 175 180

aac tgg tac aac ata aat cca tgg ata tgg ttg atg aac aag aca caa 1470
 Asn Trp Tyr Asn Ile Asn Pro Trp Ile Trp Leu Met Asn Lys Thr Gln
 185 190 195

gcc aat ctg acg gaa gga cct cca gaa aaa gaa tgc gct gtg acc tgt 1518
 Ala Asn Leu Thr Glu Gly Pro Pro Glu Lys Glu Cys Ala Val Thr Cys
 200 205 210

agg ttc gat aag gaa gca gat ata aat ata gtg aca cag gct agg gac 1566
 Arg Phe Asp Lys Glu Ala Asp Ile Asn Ile Val Thr Gln Ala Arg Asp
 215 220 225 230

agg cca aca act tta aca ggg tgt aag aaa gga aaa aaa ttt tca ttt 1614
 Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Lys Phe Ser Phe
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 Ala Gly Met Ile Ile Glu Gly Pro Cys Asn Phe Asn Val Ser Val Glu
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 Asp Ile Leu Phe Gly Asp Asn Glu Cys Ser Ser Leu Phe Gln Asp Thr
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 Ala Leu Tyr Val Val Asp Gly Val Thr Asn Thr Val Glu Asn Ala Arg
 280 285 290

caa ggg gct gca aaa ttg aca tcc tgg cta ggg aag caa ttg ggt ata 1806
 Gln Gly Ala Ala Lys Leu Thr Ser Trp Leu Gly Lys Gln Leu Gly Ile
 295 300 305 310

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 Met Gly Lys Lys Leu Glu His Lys Ser Lys Thr Trp Phe Gly Ala Asn
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 Ala Gln Ser Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Val Trp
 330 335 340

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 Tyr Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile
 345 350 355

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 Ile Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu
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cat gag atg agg ggt cat ata tgg gaa ttc att cta cta tct ttg gta 2046
 His Glu Met Arg Gly His Ile Ser Glu Phe Ile Leu Leu Ser Leu Val
 375 380 385 390

gtg cta tca gac ttc gca cct gaa aca gct agt act ctc tac ctg gtg 2094
 Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Thr Leu Tyr Leu Val
 395 400 405

cta cat ttt gcc tta cct caa acc cac gaa gtt cct agt gta tgt gac 2142

33

Leu His Phe Ala Leu Pro Gln Thr His Glu Val Pro Ser Val Cys Asp
 410 415 420
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 Thr Asn Gln Leu Asn Leu Thr Val Ser Leu Arg Val Asp Asp Val Ile
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 Pro Ser Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Val Arg Pro Asp
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 Ala Arg Thr Lys Glu Ile Gly Ala Leu Gly Ala Glu Ser Leu Thr Thr
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 Ser Val Thr Phe Glu Leu Ile Pro Gly Gly Ser Ala Met Thr Glu Glu
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 Glu Met Gly Asp Asp Phe Glu Phe Gly Leu Cys Pro Cys Asp Ser Arg
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 Pro Val Val Lys Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala
 635 640 645
 ttc caa cta ata tgc cct tac gga tgg gtc gga cgc gtg gag tgc act 2862
 Phe Gln Leu Ile Cys Pro Tyr Gly Trp Val Gly Arg Val Glu Cys Thr

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act gta agc aag agc acc ctg gca aca gag gtg gta aag ata tac aaa Thr Val Ser Lys Ser Thr Leu Ala Thr Glu Val Val Lys Ile Tyr Lys 665	670	675	2910
aag aca aaa cca ttt cca cag cgg gtt ggt tgc gac cac acc acc gtc Lys Thr Lys Pro Phe Pro Gln Arg Val Gly Cys Asp His Thr Thr Val 680	685	690	2958
tac aaa caa gac ctg tac cat tgc cag atg gga ggt aac tgg acg tgc Tyr Lys Gln Asp Leu Tyr His Cys Gln Met Gly Gly Asn Trp Thr Cys 695	700	705	3006
atg aga ggt gaa gta gtc aaa tat gtg ggg ggt cca gta aag aag tgt Met Arg Gly Glu Val Val Lys Tyr Val Gly Gly Pro Val Lys Lys Cys 715	720	725	3054
gag tgg tgc ggc tac gtg ttt aag aag aga gag ggt ctc cca cac tat Glu Trp Cys Gly Tyr Val Phe Lys Lys Arg Glu Gly Leu Pro His Tyr 730	735	740	3102
cca att ggt agg tgt atg cta aga aac gag act ggt tac aga agc gtg Pro Ile Gly Arg Cys Met Leu Arg Asn Glu Thr Gly Tyr Arg Ser Val 745	750	755	3150
gat gac aca cca tgc gat aga ggt gga gtc gtg atc agc aaa acc ggt Asp Asp Thr Pro Cys Asp Arg Gly Gly Val Val Ile Ser Lys Thr Gly 760	765	770	3198
gag ctg gaa tgc tta ata ggt aag act aca gtg aaa gta ttt agc tgc Glu Leu Glu Cys Leu Ile Gly Lys Thr Thr Val Lys Val Phe Ser Ser 775	780	785	3246
gat aaa aaa ttg gga cct atg cca tgc aga cca aaa gaa gtc ata tcc Asp Lys Lys Leu Gly Pro Met Pro Cys Arg Pro Lys Glu Val Ile Ser 795	800	805	3294
agt gaa gga cgg gtc agc aag ata gct tgc aca ttc aac tac tca aaa Ser Glu Gly Pro Val Ser Lys Ile Ala Cys Thr Phe Asn Tyr Ser Lys 810	815	820	3342
acc ctg gaa aac aaa tac tat gag ccc aga gac agt tat ttc cag caa Thr Leu Glu Asn Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln 825	830	835	3390
tac atg ctc aag gga caa tac caa tac tgg ttc gat ctt gaa gca aca Tyr Met Leu Lys Gly Gln Tyr Gln Tyr Trp Phe Asp Leu Glu Ala Thr 840	845	850	3438
gat cac cac tca gat tac ttt gca gag ttc atc atg ttg gca gtg gta Asp His His Ser Asp Tyr Phe Ala Glu Phe Ile Met Leu Ala Val Val 855	860	865	3486
gcc ctg cta ggg ggg agg tat gtc tta tgg tta atg gtt gtc tac atg Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Met Val Val Tyr Met 875	880	885	3534
atc ctg gca gat caa atg acc tca gca ata aac ctg ggc caa gga gag Ile Leu Ala Asp Gln Met Thr Ser Ala Ile Asn Leu Gly Gln Gly Glu 890	895	900	3582

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<211> 100
<212> PRT
<213> Border disease virus

<400> 14

Ser Asp Asp Asn Lys Ser Glu Lys Thr Asn Glu Lys Lys Pro Asp Arg
1 5 10 15

Val Arg Arg Gly Ala Met Lys Ile Thr Pro Lys Glu Ser Glu Lys Asp
20 25 30

Ser Arg Ser Lys Pro Pro Asp Ala Thr Ile Val Val Glu Gly Ile Lys
35 40 45

Tyr Gln Val Lys Lys Lys Gly Lys Val Lys Gly Lys Asn Thr Gln Asp
50 55 60

Gly Leu Tyr His Asn Lys Asn Lys Pro Pro Glu Ser Arg Lys Lys Leu
65 70 75 80

Glu Lys Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Phe Met Trp Glu
85 90 95

Pro Val Ala Pro
100

<210> 15
<211> 227
<212> PRT
<213> Border disease virus

<400> 15

Glu Asn Val Thr Gln Trp Asn Leu Ser Asp Asn Gly Thr Thr Gly Ile
1 5 10 15

Gln Leu Leu Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile
20 25 30

Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Thr His Leu Ala Thr Asp
35 40 45

Ala Glu Leu Lys Gly Ile Gln Gly Met Met Asp Ala Ser Glu Lys Thr
50 55 60

Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys Tyr Gly
65 70 75 80

41

Trp Cys Asn Trp Tyr Asn Ile Asn Pro Trp Ile Trp Leu Met Asn Lys
85 90 95

Thr Gln Ala Asn Leu Thr Glu Gly Pro Pro Glu Lys Glu Cys Ala Val
100 105 110

Thr Cys Arg Phe Asp Lys Glu Ala Asp Ile Asn Ile Val Thr Gln Ala
115 120 125

Arg Asp Arg Pro Thr Thr Leu Thr Gly Cys Lys Lys Gly Lys Lys Phe
130 135 140

Ser Phe Ala Gly Met Ile Ile Glu Gly Pro Cys Asn Phe Asn Val Ser
145 150 155 160

Val Glu Asp Ile Leu Phe Gly Asp Asn Glu Cys Ser Ser Leu Phe Gln
165 170 175

Asp Thr Ala Leu Tyr Val Val Asp Gly Val Thr Asn Thr Val Glu Asn
180 185 190

Ala Arg Gln Gly Ala Ala Lys Leu Thr Ser Trp Leu Gly Lys Gln Leu
195 200 205

Gly Ile Met Gly Lys Lys Leu Glu His Lys Ser Lys Thr Trp Phe Gly
210 215 220

Ala Asn Ala
225

<210> 16

<211> 195

<212> PRT

<213> Border disease virus

<400> 16

Gln Ser Pro Tyr Cys Asn Val Thr Arg Lys Ile Gly Tyr Val Trp Tyr
1 5 10 15

Thr Asn Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Ile
20 25 30

Gly Pro Gly Lys Phe Asp Thr Asn Ala Glu Asp Gly Lys Ile Leu His
35 40 45

Glu Met Arg Gly His Ile Ser Glu Phe Ile Leu Leu Ser Leu Val Val
50 55 60

Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Thr Leu Tyr Leu Val Leu
65 70 75 80

His Phe Ala Leu Pro Gln Thr His Glu Val Pro Ser Val Cys Asp Thr
85 90 95

Asn Gln Leu Asn Leu Thr Val Ser Leu Arg Val Asp Asp Val Ile Pro
 .. 200 105 110

Ser Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Val Arg Pro Asp Trp
115 120 125

Trp Pro Tyr Glu Thr Thr Met Val Leu Leu Phe Glu Glu Ala Gly Gln
130 135 140

Val Val Lys Leu Val Leu Arg Ala Ile Arg Asp Leu Thr Arg Val Trp
145 150 155 160

Asn Ser Ala Ser Thr Thr Ala Phe Leu Ile Cys Leu Val Lys Val Leu
165 170 175

Arg Gly Gln Val Val Gln Gly Leu Val Trp Leu Leu Leu Val Thr Gly
120 185 190

Ala Gln Gly
195

<210> 17

<211> 373

<212> FRT

<213> Border disease virus

<400> 27

Gln Phe Ala Cys Arg Glu Asp Tyr Arg Tyr Ala Leu Ala Arg Thr Lys
1 5 10 15

Glu Ile Gly Ala Leu Gly Ala Glu Ser Leu Thr Thr Thr Trp Thr Asp
20 25 30

Tyr Arg Gly Asn Leu Glu Leu Asp Asp Gly Thr Val Arg Ala Thr Cys
35 40 45

Ser Arg Gly Phe Phe Arg Phe Arg Gly His Cys Met Ile Gly Pro Arg
50 55 60

43

Tyr Leu Ala Ser Leu His Leu Arg Ala Leu Pro Thr Ser Val Thr Phe
65 70 75 80

Glu Leu Ile Pro Gly Gly Ser Ala Met Thr Glu Glu Glu Met Gly Asp
85 90 95

Asp Phe Glu Phe Gly Leu Cys Pro Cys Asp Ser Arg Pro Val Val Lys
100 105 110

Gly Lys Tyr Asn Thr Thr Leu Leu Asn Gly Ser Ala Phe Gln Leu Ile
115 120 125

Cys Pro Tyr Gly Trp Val Gly Arg Val Glu Cys Thr Thr Val Ser Lys
130 135 140

Ser Thr Leu Ala Thr Glu Val Val Lys Ile Tyr Lys Lys Thr Lys Pro
145 150 155 160

Phe Pro Gln Arg Val Gly Cys Asp His Thr Thr Val Tyr Lys Gln Asp
165 170 175

Leu Tyr His Cys Gln Met Gly Gly Asn Trp Thr Cys Met Arg Gly Glu
180 185 190

Val Val Lys Tyr Val Gly Gly Pro Val Lys Lys Cys Glu Trp Cys Gly
195 200 205

Tyr Val Phe Lys Lys Arg Glu Gly Leu Pro His Tyr Pro Ile Gly Arg
210 215 220

Cys Met Leu Arg Asn Glu Thr Gly Tyr Arg Ser Val Asp Asp Thr Pro
225 230 235 240

Cys Asp Arg Gly Gly Val Val Ile Ser Lys Thr Gly Glu Leu Glu Cys
245 250 255

Ile Ile Gly Lys Thr Thr Val Lys Val Phe Ser Ser Asp Lys Lys Leu
260 265 270

Gly Pro Met Pro Cys Arg Pro Lys Glu Val Ile Ser Ser Glu Gly Pro
275 280 285

Val Ser Lys Ile Ala Cys Thr Phe Asn Tyr Ser Lys Thr Leu Glu Asn
290 295 300

Lys Tyr Tyr Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr Met Leu Lys

44

305 310 315 320

Gly Gln Tyr Gln Tyr Trp Phe Asp Leu Glu Ala Thr Asp His His Ser
325 330 335

Asp Tyr Phe Ala Glu Phe Ile Met Leu Ala Val Val Ala Leu Leu Gly
340 345 350

Gly Arg Tyr Val Leu Trp Leu Met Val Val Tyr Met Ile Leu Ala Asp
355 360 365

Gln Met Thr Ser Ala
370

<210> 18

<211> 70

<212> PRT

<213> Border disease virus

<400> 18

Ile Asn Leu Gly Gln Gly Glu Val Val Leu Ile Gly Asn Leu Ile Thr
1 5 10 15

His Glu Asp His Glu Val Val Val Tyr Phe Leu Leu Leu Tyr Leu Ile
20 25 30

Val Lys Asp Glu Pro Val Lys Lys Trp Ile Leu Phe Leu Phe His Ala
35 40 45

Met Thr Asn Asn Pro Val Lys Thr Ile Ser Val Gly Leu Leu Met Leu
50 55 60

Ser Gly Leu Val Lys Gly
65 70

<210> 19

<211> 2694

<212> DNA

<213> Bovine viral diarrhea virus : deltaCErnsE1E2p7

<400> 19

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gataatgga cgcagggat accacgggca atgttccaaa ggggtgtca tagaagtlla 180

catggaatct ggccagaqza aatctgtact ggcttccctt cccatctagc caccgatata 240

gaactaaaza caatlcargg tatgatggat gcaagtgaga agaccaacta cactgtgttc 300

agacttcaac gccatgagtg gaacaagcat ggttgggtgca actggtacaa tattgaaccc 360
 tggattctag tcatgaatag aacccaagcc aatctcactg agggacaacc accaagggag 420
 tgggcagtc cttgtaggta tgatagggct agtgacttaa acgtggtaac acaagctaga 480
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<210> 20
<211> 900
<212> PRT
<213> Bovine viral diarrhea virus : deltaCErnsE1E2p7

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<222> (1)..(34)
<223> core protein

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<222> (35)..(261)
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<223> E1

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<223> E1

<220>
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<222> (157)..(330)
<223> E2

<220>
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<222> (831)..(900)
<223> p7

<100> 20

Met Asn Ser Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys
1 5 10 15

47

Ala Leu Leu Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr
 20 25 30

Met Gly Glu Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu
 35 40 45

Gly Ile Gln Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His
 50 55 60

Gly Ile Trp Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala
 65 70 75 80

Thr Asp Ile Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu
 85 90 95

Lys Thr Asn Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys
 100 105 110

His Gly Trp Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met
 115 120 125

Asn Arg Thr Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys
 130 135 140

Ala Val Thr Cys Arg Tyr Asp Arg Ala Ser Asp Leu Asn Val Val Thr
 145 150 155 160

Gln Ala Arg Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys
 165 170 175

Asn Phe Ser Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu
 180 185 190

Ile Ala Ala Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met
 195 200 205

Phe Gln Asp Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu
 210 215 220

Glu Gly Ala Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys
 225 230 235 240

Gln Leu Gly Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp
 245 250 255

Phe Gly Ala Tyr Ala Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile
260 265 270

Gly Tyr Ile Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys
275 280 285

Asn Thr Lys Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp
290 295 300

Gly Lys Ile Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu Leu
305 310 315 320

Leu Ser Leu Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val
325 330 335

Met Tyr Leu Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp Val
340 345 350

Met Asp Cys Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr
355 360 365

Ala Glu Val Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys
370 375 380

Ile Arg Pro Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe
385 390 395 400

Glu Glu Val Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp
405 410 415

Leu Thr Arg Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys
420 425 430

Leu Val Lys Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu
435 440 445

Leu Leu Ile Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu Phe
450 455 460

Ser Tyr Ala Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu
465 470 475 480

Gly Leu Thr Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu
485 490 495

49

Asp Thr Met Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu
 500 505 510

Gln Arg Cys Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His Thr Arg
 515 520 525

Ala Leu Pro Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg Lys
 530 535 540

Gln Glu Asp Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu Cys
 545 550 555 560

Pro Cys Asp Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr Leu
 565 570 575

Leu Asn Gly Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr Gly
 580 585 590

Thr Val Ser Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr Val
 595 600 605

Val Arg Thr Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly Cys
 610 615 620

Ile Thr Gln Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu Gly
 625 630 635 640

Gly Asn Trp Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly
 645 650 655

Ser Ile Glu Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu
 660 665 670

Gly Leu Pro His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr
 675 680 685

Gly Tyr Arg Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val Ala
 690 695 700

Ile Val Pro Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr Val
 705 710 715 720

Gln Val Ile Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg Pro
 725 730 735

Tyr Glu Ile Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys Thr

50

740

745

750

Phe Asn Tyr Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp
755 760 765

Ser Tyr Phe Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe
770 775 780

Asp Leu Glu Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser Ile
785 790 795 800

Leu Val Val Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu
805 810 815

Leu Val Thr Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly Ile Gln
820 825 830

Tyr Gly Ser Gly Glu Val Val Met Met Gly Asn Leu Leu Thr His Asn
835 840 845

Asn Ile Glu Val Val Thr Tyr Phe Leu Leu Leu Tyr Leu Leu Leu Arg
850 855 860

Glu Glu Ser Val Lys Lys Trp Val Leu Leu Leu Tyr His Ile Leu Val
865 870 875 880

Val His Pro Ile Lys Ser Val Ile Val Ile Leu Leu Met Ile Gly Asp
885 890 895

Val Val Lys Ala
900

<210> 21

<211> 2484

<212> DNA

<213> Bovine viral diarrhea virus : delraCERNsE1E2

<400> 21

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gataatggga cggagaggat acaacgggca atgttccaaa ggggtgtgaa tagaagttta 180

catggaatct ggccagagaa aatctgtact gggttcctt cccatctagc caccgatata 240

gaactaaaa caattcatgg tangatggat gcaagtga agacaaacta caagtgttgc 300

agatttcaac gcaatgagtg gaacaagcat ggttgggtga actgttataa tattgaaccc 360

tggattctag tcatgaatag aacccaagcc aatctcactg agggacaacc accaugggag 420
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<210> 22
 <211> 827
 <212> PRT
 <213> Bovine viral diarrhea virus : deltaCERNsE122

<400> 22

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
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Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Glu
 20 25 30

Asn Ile Thr Gln Trp Asn Leu Gln Asp Asn Gly Thr Glu Gly Ile Gln
 35 40 45

Arg Ala Met Phe Gln Arg Gly Val Asn Arg Ser Leu His Gly Ile Trp
 50 55 60

Pro Glu Lys Ile Cys Thr Gly Val Pro Ser His Leu Ala Thr Asp Ile
 65 70 75 80

Glu Leu Lys Thr Ile His Gly Met Met Asp Ala Ser Glu Lys Thr Asn
 85 90 95

Tyr Thr Cys Cys Arg Leu Gln Arg His Glu Trp Asn Lys His Gly Trp
 100 105 110

Cys Asn Trp Tyr Asn Ile Glu Pro Trp Ile Leu Val Met Asn Arg Thr
 115 120 125

Gln Ala Asn Leu Thr Glu Gly Gln Pro Pro Arg Glu Cys Ala Val Thr
 130 135 140

Cys Arg Tyr Asp Arg Ala Ser Asp Ile Asn Val Val Thr Gln Ala Arg
 145 150 155 160

Asp Ser Pro Thr Pro Leu Thr Gly Cys Lys Lys Gly Lys Asn Phe Ser
 165 170 175

Phe Ala Gly Ile Leu Met Arg Gly Pro Cys Asn Phe Glu Ile Ala Ala
180 185 190

Ser Asp Val Leu Phe Lys Glu His Glu Arg Ile Ser Met Phe Gln Asp
195 200 205

Thr Thr Leu Tyr Leu Val Asp Gly Leu Thr Asn Ser Leu Glu Gly Ala
210 215 220

Arg Gln Gly Thr Ala Lys Leu Thr Thr Trp Leu Gly Lys Gln Leu Gly
225 230 235 240

Ile Leu Gly Lys Lys Leu Glu Asn Lys Ser Lys Thr Trp Phe Gly Ala
245 250 255

Tyr Ala Ala Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile
260 265 270

Trp Tyr Thr Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys
275 280 285

Ile Val Gly Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile
290 295 300

Leu His Glu Met Gly Gly His Leu Ser Glu Val Leu Leu Ser Leu
305 310 315 320

Val Val Leu Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu
325 330 335

Ile Leu His Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys
340 345 350

Asp Lys Thr Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val
355 360 365

Ile Pro Gly Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro
370 375 380

Asn Trp Trp Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val
385 390 395 400

Ser Gln Val Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg
405 410 415

Ile Trp Asn Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys
420 425 430

Ile Val Arg Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Ile
435 440 445

Thr Gly Val Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala
450 455 460

Ile Ala Lys Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr
465 470 475 480

Thr Thr Trp Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met
485 490 495

Val Ile Ala Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys
500 505 510

Thr Arg Glu Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro
515 520 525

Thr Ser Val Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp
530 535 540

Val Val Glu Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp
545 550 555 560

Ala Lys Pro Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly
565 570 575

Pro Ala Phe Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser
580 585 590

Cys Thr Ser Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr
595 600 605

Tyr Arg Arg Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln
610 615 620

Lys Asn Leu Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp
625 630 635 640

Thr Cys Val Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu
645 650 655

55

Ser Cys Lys Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro
660 665 670

His Tyr Pro Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg
675 680 685

Leu Val Asp Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro
690 695 700

Gln Gly Thr Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile
705 710 715 720

Ala Met Asp Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile
725 730 735

Ile Ser Ser Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr
740 745 750

Thr Lys Thr Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe
755 760 765

Gln Gln Tyr Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu
770 775 780

Val Thr Asp His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val
785 790 795 800

Val Val Ala Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr
805 810 815

Tyr Met Val Leu Ser Glu Gln Lys Ala Leu Gly
820 825

<210> 23

<211> 2013

<212> DNA

<213> Bovine viral diarrhea virus : deltaCE1E2p7

<400> 23

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atgggggggtc acttctcgga ggtactacta ctctcttttag tgggtctgtc cgacttcgca 300
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<210> 24
<211> 670
<212> FRT

57

<213> Bovine viral diarrhea virus : deltaCE1E2p7

<400> 24

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
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Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Ala
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Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr Thr
35 40 45

Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val Gly
50 55 60

Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu
65 70 75 80

Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val Leu
85 90 95

Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu His
100 105 110

Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys Thr
115 120 125

Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro Gly
130 135 140

Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp Trp
145 150 155 160

Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln Val
165 170 175

Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp Asn
180 185 190

Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val Arg
195 200 205

Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly Val
210 215 220

Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys

58

225 230 235 240
 Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp
 245 250 255

 Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala
 260 265 270

 Trp-Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu
 275 280 285

 Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val
 290 295 300

 Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu
 305 310 315 320

 Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro
 325 330 335

 Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe
 340 345 350

 Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser
 355 360 365

 Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg
 370 375 380

 Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu
 385 390 395 400

 Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val
 405 410 415

 Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys
 420 425 430

 Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro
 435 440 445

 Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp
 450 455 460

 Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr
 465 470 475 480

59

Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp
485 490 495

Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser
500 505 510

Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr
515 520 525

Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
530 535 540

Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp
545 550 555 560

His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala
565 570 575

Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val
580 585 590

Leu Ser Glu Gln Lys Ala Leu Gly Ile Gln Tyr Gly Ser Gly Glu Val
595 600 605

Val Met Met Gly Asn Leu Leu Thr His Asn Asn Ile Glu Val Val Thr
610 615 620

Tyr Phe Leu Leu Leu Tyr Leu Leu Leu Arg Glu Glu Ser Val Lys Lys
625 630 635 640

Trp Val Leu Leu Leu Tyr His Ile Leu Val Val His Pro Ile Lys Ser
645 650 655

Val Ile Val Ile Leu Leu Met Ile Gly Asp Val Val Lys Ala
660 665 670

<210> 25
<211> 1803
<212> DNA
<213> Bovine viral diarrhea virus : deltaCE1E2

<400> 25
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aaaattggct acatatggta tacaaaaaat tgcacccctg cctgcttacc caagaacaca 180

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 gatgtaacgg attgtgataa gaccagttg aacctcacag tggagctgac aacagctgaa 420
 gtaataccag ggtcgggtctg gaattctaggc aaatatgtat gtataagacc aaattgggtg 480
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 agatatgtac tttggttact ggttacatc atggtcttat cagaacagaa ggccttaggg 1800
 tga 1803

<210> 26
 <211> 600
 <212> PRT

<213> Bovine viral diarrhea virus : deltaCE1E2

<400> 26

Lys Asn Lys Pro Gln Glu Ser Arg Lys Lys Leu Glu Lys Ala Leu Leu
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Ala Trp Ala Ile Ile Ala Ile Val Leu Phe Gln Val Thr Met Gly Ala
20 25 30

Ser Pro Tyr Cys Asp Val Asp Arg Lys Ile Gly Tyr Ile Trp Tyr Thr
35 40 45

Lys Asn Cys Thr Pro Ala Cys Leu Pro Lys Asn Thr Lys Ile Val Gly
50 55 60

Pro Gly Lys Phe Gly Thr Asn Ala Glu Asp Gly Lys Ile Leu His Glu
65 70 75 80

Met Gly Gly His Leu Ser Glu Val Leu Leu Leu Ser Leu Val Val Leu
85 90 95

Ser Asp Phe Ala Pro Glu Thr Ala Ser Val Met Tyr Leu Ile Leu His
100 105 110

Phe Ser Ile Pro Gln Ser His Val Asp Val Met Asp Cys Asp Lys Thr
115 120 125

Gln Leu Asn Leu Thr Val Glu Leu Thr Thr Ala Glu Val Ile Pro Gly
130 135 140

Ser Val Trp Asn Leu Gly Lys Tyr Val Cys Ile Arg Pro Asn Trp Trp
145 150 155 160

Pro Tyr Glu Thr Thr Val Val Leu Ala Phe Glu Glu Val Ser Gln Val
165 170 175

Val Lys Leu Val Leu Arg Ala Leu Arg Asp Leu Thr Arg Ile Trp Asn
180 185 190

Ala Ala Thr Thr Thr Ala Phe Leu Val Cys Leu Val Lys Ile Val Arg
195 200 205

Gly Gln Met Val Gln Gly Ile Leu Trp Leu Leu Leu Ile Thr Gly Val
210 215 220

Gln Gly His Leu Asp Cys Lys Pro Glu Phe Ser Tyr Ala Ile Ala Lys

62

225	230	235	240
Asp Glu Arg Ile Gly Gln Leu Gly Ala Glu Gly Leu Thr Thr Thr Trp	245	250	255
Lys Glu Tyr Ser Pro Gly Met Lys Leu Glu Asp Thr Met Val Ile Ala	260	265	270
Trp Cys Glu Asp Gly Lys Leu Met Tyr Leu Gln Arg Cys Thr Arg Glu	275	280	285
Thr Arg Tyr Leu Ala Ile Leu His Thr Arg Ala Leu Pro Thr Ser Val	290	295	300
Val Phe Lys Lys Leu Phe Asp Gly Arg Lys Gln Glu Asp Val Val Glu	305	310	315
Met Asn Asp Asn Phe Glu Phe Gly Leu Cys Pro Cys Asp Ala Lys Pro	325	330	335
Ile Val Arg Gly Lys Phe Asn Thr Thr Leu Leu Asn Gly Pro Ala Phe	340	345	350
Gln Met Val Cys Pro Ile Gly Trp Thr Gly Thr Val Ser Cys Thr Ser	355	360	365
Phe Asn Met Asp Thr Leu Ala Thr Thr Val Val Arg Thr Tyr Arg Arg	370	375	380
Ser Lys Pro Phe Pro His Arg Gln Gly Cys Ile Thr Gln Lys Asn Leu	385	390	395
Gly Glu Asp Leu His Asn Cys Ile Leu Gly Gly Asn Trp Thr Cys Val	405	410	415
Pro Gly Asp Gln Leu Leu Tyr Lys Gly Gly Ser Ile Glu Ser Cys Lys	420	425	430
Trp Cys Gly Tyr Gln Phe Lys Glu Ser Glu Gly Leu Pro His Tyr Pro	435	440	445
Ile Gly Lys Cys Lys Leu Glu Asn Glu Thr Gly Tyr Arg Leu Val Asp	450	455	460
Ser Thr Ser Cys Asn Arg Glu Gly Val Ala Ile Val Pro Gln Gly Thr	465	470	475
			480

Leu Lys Cys Lys Ile Gly Lys Thr Thr Val Gln Val Ile Ala Met Asp
 485 490 495

Thr Lys Leu Gly Pro Met Pro Cys Arg Pro Tyr Glu Ile Ile Ser Ser
 500 505 510

Glu Gly Pro Val Glu Lys Thr Ala Cys Thr Phe Asn Tyr Thr Lys Thr
 515 520 525

Leu Lys Asn Lys Tyr Phe Glu Pro Arg Asp Ser Tyr Phe Gln Gln Tyr
 530 535 540

Met Leu Lys Gly Glu Tyr Gln Tyr Trp Phe Asp Leu Glu Val Thr Asp
 545 550 555 560

His His Arg Asp Tyr Phe Ala Glu Ser Ile Leu Val Val Val Val Ala
 565 570 575

Leu Leu Gly Gly Arg Tyr Val Leu Trp Leu Leu Val Thr Tyr Met Val
 580 585 590

Leu Ser Glu Gln Lys Ala Leu Gly
 595 600